Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims

1. (Currently amended) A method for analysing a heterogeneous sample comprising a mixture of proteins, peptides, protein fragments or peptide fragments, the method comprising:

   (a) separating the heterogeneous sample of proteins, peptides, protein fragments or peptide fragments, into heterogeneous classes by binding the members of each class to ~~a~~ antibodies or fragments thereof, each antibody, or fragment thereof, fixed to spaced apart defined ~~location~~ locations on an array, wherein more than one protein, peptide, protein fragment or peptide fragment binds to each defined location on the array, and wherein those proteins, peptides, or protein fragments or peptide fragments binding to a specific antibody represent a heterogenous class and the members of each class have a motif common to that class; and

   (b) characterising all the proteins, peptides, protein fragments or peptide fragments~~,~~ in each class by determining the mass of the proteins, peptides, protein fragments or peptide fragments in each of the heterogeneous classes, and determining the abundance of proteins, peptides, protein fragments or peptide fragments, of different mass in the heterogeneous classes, wherein the characterization is conducted using mass spectrometry.

2. (Previously presented) A method according to claim 1 wherein the heterogeneous sample of proteins, peptides, protein fragments or peptide fragments, is an extract of the total protein content of a cell or tissue type.

3. (Previously presented) A method according to claim 1 wherein, prior to performing step (a), the proteins and peptides in the heterogeneous sample are fragmented to form protein fragments and peptide fragments.

4. (Previously presented) A method according to claim 3 wherein the fragmenting is

performed by chemical or enzymatic cleavage.

5. (Previously presented) A method according to claim 3 wherein the fragmenting is performed using a sequence-directed cleavage mechanism.

6. (Previously presented) A method according to claim 3 wherein the fragmenting is performed by digestion of the heterogeneous sample of proteins or peptides with trypsin.

7. (Previously presented) A method according to claim 1 wherein the motif in each peptide, or protein or peptide fragment, is at the same location in each peptide, or protein or peptide fragment, relative to the C-terminus, the N-terminus, or an internal feature.

8. (Previously presented) A method according to claim 1 wherein the heterogeneous sample is a heterogeneous sample of protein fragments or peptide fragments and the motif in each fragment is at the same location in each fragment, relative to the site of cleavage.

9. (Previously presented) A method according to claim 1 wherein the motif in each peptide, or protein or peptide fragment, is three, four, five, six or more amino acids in length.

10. (Previously presented) A method according to claim 1 wherein the motif contains three, four or five variable amino acids, the other amino acids in the motif being constant between all peptides, or protein or peptide fragments.

11. (Previously presented) A method according claim 1 wherein the motif is at the C-terminus.

12. (Withdrawn) A method according to claim 1 wherein the motif is at the N-terminus.

13. (Currently amended) A method according to claim 1 wherein the array comprises a number of different types of ~~binding molecule~~ antibody, each type immobilised at a spaced apart defined location on the array, wherein each type of ~~binding molecule~~

antibody is capable of binding specifically to a motif and wherein different types of ~~binding molecule~~ antibody have different binding specificities.

14. (Currently amended) A method according to claim 3 wherein the number of different types of ~~binding molecule~~ antibody provided on the array is suitable to capture at least 10% of the peptides in the heterogeneous sample prior to fragmentation or, where the sample is a heterogeneous sample of protein fragments or peptide fragments, at least one fragment from at least 10% of the proteins or peptides in the unfragmented heterogeneous sample.

15. (Withdrawn) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture at least 50% of the proteins or peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from at least 50% of the proteins or peptides in the unfragmented sample.

16. (Withdrawn) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture substantially 100% of the proteins or peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from substantially 100% of the proteins or peptides in the unfragmented sample.

17. (Currently amended) A method according to claim 13 wherein the array has at least about 10, 50, 100, 150, 200, 250, 300, or more different types of ~~binding molecule~~ antibody provided thereon.

18. Cancelled.

19. (Withdrawn) A method according to claim 13 wherein at least one of the types of the binding molecule is an aptamer.

20. (Withdrawn) A method according to claim 13 wherein at least one of the types of the binding molecule is a polynucleotide.

21. (Previously presented) A method according to claim 1 wherein step (b) comprises characterizing bound peptides, or protein or peptide fragments, at the defined and discrete locations on the array.

22. (Canceled)

23. (Canceled)

24. (Previously presented) A method according to claim 1 wherein step (b) comprises characterizing the peptides, or protein or peptide fragments, in the heterogeneous classes by desorption mass spectrometry or collision induced dissociation mass spectrometry.

25. (Canceled)

26. (Previously presented) A method according to claim 3 wherein the information derived from step (b) is used to determine the abundance of the protein or peptide in the heterogeneous sample from which the protein fragment or peptide fragment is derived.

27. (Previously presented) A method for identifying differences in composition between two or more heterogeneous fragmented or unfragmented samples of proteins, peptides, protein fragments or peptide fragments, comprising analysing each sample by the method according to claim 1 and comparing the results, thereby to identify any differences.

Claims 28-49 (canceled).